MODELING THE EFFECTIVENESS OF ISOLATION STRATEGIES IN PREVENTING STD EPIDEMICS[*]

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Abstract. We formulate and analyze a two-group, selective-mixing, susceptible-infective-susceptible (SIS), sexually transmitted disease (STD) model where the infection-dependent desirability and acceptability in partnership formations are zero at high infection levels. We analyze two strategies to limit the spread of the epidemic by avoiding forming partnerships with people in a highly infected group. In one approach, the people in the highly infected group protect themselves by forming partnerships with only people outside their own group. We show that the transmission dynamics for this approach are similar to the situation where people continue to have both intragroup and intergroup partnerships. In the second approach, when one group becomes highly infected, the people in the other group adopt an isolation strategy and stop forming any partnerships with people in this highly infected group. We show that the second approach can limit the epidemic to the highly infected group. The other group will be infection-free, but as long as the epidemic in the total population exceeds the epidemic threshold, the epidemic will continue to persist. If the group reproductive number of the infection-free group is greater than one, and the infection should ever invade the infection-free group, then it will lead to an epidemic similar to the one that would have occurred if they had not isolated themselves from the other group. In this simple two-group model, although these isolation strategies may reduce the extent of an STD epidemic, they are ineffective in preventing an epidemic.

Key words. sexually transmitted disease models, selective mixing, partner formations, behavior changes, reproductive numbers, endemic equilibrium, local stability, global stability

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1. Introduction. Mathematical models can give insight into the future course of STD epidemics. For these models to be accurate, they must account for sexual behavior changes that occur while the epidemic is in progress. Substantial sexual behavior changes have been documented in virtually every survey over the last decade [1, 5, 15, 16]. The behavioral changes in homosexual men and intravenous drug users may partially be due to the increased awareness of the fatal feature of human immunodeficiency virus (HIV) infection in devising education plans. Some survey studies and analyses have suggested that the reported behavior changes combined with an observed reduction in the incidence of rectal gonorrhea have been large enough to reduce the rate of HIV transmission, and the researchers have expressed hope that the changes may be sufficient to reduce the rate of HIV transmission below the epidemic threshold [5, 11, 25].

Our goal is to incorporate these behavior changes into a mathematical model to help us understand the transmission dynamics of STD epidemics and to provide guid-

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ance into the effective strategies in preventing or reducing the impact of an epidemic in multigroup populations.

Most of the epidemiological models used to analyze behavior changes are simple compartmental STD models (see, e.g., [6, 7, 24]) and the analysis has focused on the epidemic threshold [2, 13, 17, 19, 20, 22, 23]. The investigations that do include behavior changes are often performed by using different sets of parameters and simulating the model for the whole course of the epidemic. Because of the complexity of the transmission dynamics of STDs and the difficulty in the mathematical analysis, these models usually assume that the dynamics of partnership formations do not change during the simulation.

Human behaviors are complicated, involving both social and physiological factors. People do change their behavior in response to an epidemic, and these changes should be accounted for dynamically in the model. In many multigroup models the complexities of enforcing the balance constraints for partnership formations have limited the consideration of such dynamical changes in partnership formations. However, in selective-mixing models, the balance constraints are automatically satisfied even for dynamically changing partnership formations, making these models ideal to study the effects of behavior changes on the STD epidemics [9, 12].

In a previous paper [10], we investigated the effectiveness of limiting the spread of STDs by dividing the population into groups and restricting the partnership formations between individuals in these groups based on the fraction of each infected group. These groups may be considered as consisting of people living in separate geographic, social, economic, or ethnic communities. We assumed that people in each group use information about the fraction of infected people in each of the groups to determine the desirability and acceptability of their possible partners and reduce the desirability and acceptability as the fraction of infected people increases. The hope was that if all the people significantly reduced forming partnerships with people in the group where there was a high infection level, it would stop the epidemic. However, we showed, in [10], that as long as people continued to form intragroup and intergroup partnerships, no matter how high the level of infection was in a group, this strategy was not effective in stopping an epidemic.

In this paper, we extend the results in [10] by analyzing how the dynamics of the epidemic would change if the people in a group were to stop forming any partnerships with people in the highly infected group. This is accomplished by allowing the acceptability and desirability functions to be zero for highly infected groups.

We formulate a two-group, selective-mixing, SIS STD model with infection-dependent desirability and acceptability in the partnership formations, similar to the models proposed in [9] and [12]:

(1.1)
$$\begin{cases} \dfrac{dS_i}{dt} = \mu(S_i^0 - S_i) - \lambda_i S_i + \gamma_i I_i, \\[2mm] \dfrac{dI_i}{dt} = -(\mu + \gamma_i)I_i + \lambda_i S_i, \end{cases} \quad i = 1, 2,$$

where S_i and I_i are the susceptible and infected populations in the ith group, μ is the natural death rate, γ_i is the rate of recovery for infected individuals in group i, μS_i^0 is the rate of recruitment into group i, and λ_i is the rate of infection given by

$$\lambda_i = c_i \sum_{j=1}^{2} \beta_{ij} q_{ij}\left(\frac{I_j}{N_j}\right) q_{ji}\left(\frac{I_i}{N_i}\right) \frac{c_j I_j}{\sum\limits_{k} c_k N_k}.$$

Here c_i is the number of social contacts per unit time for a person in group i, β_{ij} is the probability of disease transmission per contact between a susceptible individual in group i and an infected partner in group j, $N_i = S_i + I_i$ is the size of the population in group i, and I_i/N_i is the fraction of the infected population in group i. This fraction is also the probability of having a partner from group i who is infected. The nonnegative function q_{ij} is the desirability of people in group i to have a partner from group j and the acceptability of people in group j to form a partnership with people in group i. We assume that people make their selections according to the infection level in the group in which they attempt to form partnerships and that $q_{ij}(I_j/N_j)$ is a decreasing function of I_j/N_j.

In [10] we proved that as long as people continue to have intragroup and intergroup partnership formations, a simple switch of partners between groups or a temporary decrease in the number of partners cannot eradicate an epidemic. That is, as the reproductive number R_0 is less than one, the epidemic dies out, and as R_0 is greater than one, the endemic spreads in the population regardless of the initial infection status.

The condition that the infection-dependent desirability and acceptability functions are always positive implies that people will always have some intragroup and intergroup partnerships. This positivity assumption may be reasonable in very high risk communities, but it is equally realistic to assume that when the fractions of infectives are sufficiently high, people may temporarily stop forming any partnerships at all with people in highly infected groups. Historically, communities have tried to isolate themselves from infectious diseases by eliminating or minimizing contacts with people in other communities or groups that are infected with the disease. Sometimes this isolation policy is combined with an attempt to quarantine the infected individuals to prevent them from infecting others.

To understand how this isolation approach affects the course of an epidemic, we will investigate the effects of behavior changes on the dynamics of the two-group SIS STD models where we relax the positivity constraint to $q_{ij} \geq 0$. That is, we allow the preference functions to become zero when the fraction of infectives in a group is high. We will completely analyze the cases where the partnership formations within the groups or the partnerships between the two groups are stopped at high infection levels.

2. Model analysis. System (1.1) is equivalent to the following system:

(2.1)
$$\begin{cases} \dfrac{dN_i}{dt} = \mu S_i^0 - \mu N_i, \\[2mm] \dfrac{dI_i}{dt} = -(\mu + \gamma_i)I_i + \lambda_i(N_i - I_i), \end{cases} \qquad i = 1, 2.$$

Since $\lim_{t\to\infty} N_i = S_i^0$, the limiting system of (2.1) is

(2.2)
$$\frac{dI_i}{dt} = -\left(\mu + \gamma_i\right) I_i + \lambda_i \left(S_i^0 - I_i\right), \qquad i = 1, 2,$$

where

$$\lambda_i = \frac{c_i}{N^0} \sum_{j=1}^{2} q_{ij}\left(\frac{I_j}{S_j^0}\right) q_{ji}\left(\frac{I_i}{S_i^0}\right) \beta_{ij} c_j I_j$$

with $N^0 := c_1 S_1^0 + c_2 S_2^0$.

The dynamics of (2.1) can be qualitatively determined by the dynamics of (2.2) [4, 21]. Define $y_i := I_i/S_i^0$ and denote

(2.3)
$$w_i(y_i) := p_{ii} = q_{ii}^2(y_i), \qquad i = 1, 2,$$
$$g(y_2) := q_{12}(y_2),$$
$$h(y_1) := q_{21}(y_1),$$

where $w_i, g, h : \mathbb{R} \to [0, \infty)$ are piecewise differentiable and decreasing functions. The system (2.2) can be transformed into

(2.4)
$$\frac{dy_i}{dt} = -(\mu + \gamma_i)y_i + \lambda_i(1 - y_i), \qquad i = 1, 2,$$

with

$$\lambda_i = \frac{c_i}{N^0}\left(\beta_{ii}c_i S_i^0 w_i(y_i)y_i + \beta_{ij}c_j S_j^0 h(y_1)g(y_2)y_j\right),$$

where $j \neq i$. Hereinafter we will study the transformed system.

2.1. Previous results. We briefly state the fundamental results on the dynamical behavior of the model (2.4) proved in [10], which will be used in the following sections. First, we have an explicit formula for the reproductive number.

THEOREM 2.1. *The reproductive number can be defined by*

(2.5) $\quad R_0 = \dfrac{1}{(2\mu + \gamma_1 + \gamma_2)N^0}\left(\alpha_{11} + \alpha_{22} + \sqrt{(\gamma_1 - \gamma_2 + \alpha_{22} - \alpha_{11})^2 + 4\alpha_{12}\alpha_{21}}\right),$

where

$$\alpha_{11} = S_1^0 c_1^2 \beta_{11} w_1(0), \qquad \alpha_{12} = S_1^0 c_1 c_2 \beta_{12} h(0)g(0),$$

$$\alpha_{21} = S_2^0 c_1 c_2 \beta_{21} h(0)g(0), \qquad \alpha_{22} = S_2^0 c_2^2 \beta_{22} w_2(0).$$

If $R_0 < 1$, the infection-free equilibrium $(y_1, y_2) = (0, 0)$ is globally stable, which implies that the epidemic dies out regardless of initial infection status. If $R_0 > 1$, the infection-free equilibrium is unstable, which results in the spread of the disease in the population.

Then we have the following lemmas, which will be used in this paper again to determine the global dynamics of (2.4).

LEMMA 2.2. *Define the set $D := \{(y_1, y_2) \in [0, 1] \times [0, 1]\}$. Then D is a global attractor for (2.4) in the nonnegative first quadrant; the nonnegative first quadrant is forward invariant under the flow defined by (2.4), and all orbits defined by (2.4) are bounded for all time $t \geq 0$.*

LEMMA 2.3. *The plan autonomous system (2.4) has neither limit cycles nor closed phase polygons in the positive quadrant.*

To investigate the uniqueness of the solution, we define functions F_i such that the zeros of F_i correspond to steady states of (2.4).

LEMMA 2.4. *Let*

$$F_i(y_1, y_2) := c_i(1 - y_i)\left(\beta_{ii}c_i S_i^0 w_i(y_i)y_i + \beta_{ij}c_j S_j^0 h(y_1)g(y_2)y_j\right) - (\mu + \gamma_i)N^0 y_i$$
(2.6)
for $i = 1, 2$, $j \neq i$, and $y_i \geq 0$. The curve $F_1(y_1, y_2) = 0$ or $F_2(y_1, y_2) = 0$ only intersects the ray $y_2 = ky_1$, $y_1 > 0$, at most once for any positive real number $k > 0$.

We also show that, for the two-group model, if the desirability and acceptability function is strictly positive, then there are only two kinds of equilibria in the two-group model: the infection-free equilibrium and the positive endemic equilibrium. If R_0 is less than one, the infection-free equilibrium is the only equilibrium and it is globally stable. If $R_0 > 1$, the infection-free equilibrium is unstable and the positive endemic equilibrium is globally stable.

Then the following question arises: if people completely stop partnership formations as the infection level becomes high, do these behavior changes have significant impacts on the transmission dynamics? We investigate this question in the following two sections.

2.2. Persistent intergroup partner formations. In this section we assume that people use information about the infection within their own group such that when the fraction of infectives reaches a certain level, they stop forming partnerships within the group. However, they always desire partnerships and accept partners from people in the other group. (This may be because they have less accurate information about the infection level in the other group.) We assume that the intergroup desirability and acceptability functions $g(x)$ and $h(x)$ are strictly positive and decreasing functions for all $x \geq 0$, and that there exist positive numbers $0 < m_i < 1$, $i = 1, 2$, such that the intragroup desirability and acceptability functions satisfy

$$(2.7) \qquad\qquad w_i(x) \begin{cases} > 0, & 0 \leq x < m_i, \\ = 0, & m_i \leq x \leq 1. \end{cases}$$

A different feature of the dynamics of model (2.4) with desirability and acceptability becoming zero as infection level is high is that there is a possibility of the existence of boundary equilibria, one of whose components is positive and the other is zero ($(y_1^0 > 0, y_2^0 = 0)$ or $(y_1^0 = 0, y_2^0 > 0)$). However, if intergroup desirability and acceptability functions are strictly positive, boundary equilibria do not exist.

Any equilibrium must satisfy $F_i(y_1, y_2) = 0$, $i = 1, 2$. If there exists a boundary equilibrium $(y_1 > 0, y_2 = 0)$, then, because $F_2(y_1, y_2) = 0$ at any equilibrium, it follows that

$$(2.8) \qquad\qquad c_2 \beta_{21} c_1 S_1^0 h(y_1) g(0) y_1 = 0.$$

Since h and g are strictly positive, (2.8) has no nonzero solution.

Then, using the same arguments as in [10], we have the following results.

THEOREM 2.5. *Suppose that the intragroup partnership formations w_i are decreasing functions satisfying the assumption (2.7), and that the intergroup partnership formations g and h are strictly positive decreasing functions. Then if $R_0 < 1$ the infection-free equilibrium is the only equilibrium and is globally stable in the positive quadrant $y_1 > 0$, $y_2 > 0$; that is, all solutions starting in the positive quadrant have $\lim_{t \to \infty}(y_1(t), y_2(t)) = (0, 0)$. If $R_0 > 1$, the infection-free equilibrium is unstable, and there exists a unique positive endemic equilibrium $(0 < y_1^* < 1, 0 < y_2^* < 1)$, which is globally stable in the positive quadrant; that is, all solutions starting in the positive quadrant have $\lim_{t \to \infty}(y_1(t), y_2(t)) = (y_1^*, y_2^*)$.*

We only give an outline of the proof since it is similar to the one presented in [10]. First, based on Lemma 2.4, it can be shown that if $R_0 < 1$, there is no intersection of the curves $F_1(y_1, y_2) = 0$ and $F_2(y_1, y_2) = 0$ in the nonnegative first quadrant except $y_1 = y_2 = 0$, and if $R_0 > 1$, there exists a unique intersection of the two curves in the positive quadrant. Second, if $R_0 < 1$, since the infection-free equilibrium is

the only equilibrium in the nonnegative first quadrant including the y_1 and y_2 axes, Lemmas 2.2 and 2.3 lead to the global stability of the infection-free equilibrium in the nonnegative first quadrant. If $R_0 > 1$, since the infection-free equilibrium becomes unstable and the positive endemic equilibrium is unique in the positive quadrant, again, based on Lemmas 2.2 and 2.3, we conclude the global stability of the positive endemic equilibrium.

2.3. Possible break in intergroup partner formations. In this section we consider the situation where when one group becomes highly infected, people in the other group stop forming partnerships with them. That is, we assume that $w_i(x)$, $i = 1, 2$, are strictly positive decreasing functions for all $x \geq 0$, and that there exist positive numbers $0 < k_i < 1$, $i = 1, 2$, such that

$$(2.9) \qquad h(x) \begin{cases} > 0, & 0 \leq x < k_1, \\ = 0, & k_1 \leq x \leq 1, \end{cases} \qquad \text{and} \qquad g(x) \begin{cases} > 0, & 0 \leq x < k_2, \\ = 0, & k_2 \leq x \leq 1. \end{cases}$$

Then boundary equilibria may exist.

LEMMA 2.6. *Let*

$$R_i(x) := \frac{w_i(x) c_i^2 \beta_{ii} S_i^0}{(\mu + \gamma_i) N^0}$$

and $H_i(x) := (1 - x) R_i(x)$. Define the group reproductive number for group i to be $R_i(0)$.

(1) There exists a boundary equilibrium $(y_i^0 = 0, y_j^0 > 0)$, $j \neq i$, if and only if $H_j(k_j) \geq 1$. Moreover, if it exists, it is unique on that axis, and $y_j^0 \geq k_j$.

(2) Suppose that the boundary equilibrium $(y_i^0 = 0, y_j^0 \geq k_j)$, $j \neq i$, exists. Then it is locally stable if $R_i(0) < 1$, and it is unstable if $R_i(0) > 1$.

Proof. (1) It follows from at any equilibrium,

$$c_i \left(1 - y_i \right) \left(\beta_{ii} c_i S_i^0 w_i(y_i) y_i + \beta_{ij} c_j S_j^0 h(y_1) g(y_2) y_j \right) = (\mu + \gamma_i) N^0 y_i,$$

that there are no boundary equilibria $(y_i^0 = 0, y_j^0 > 0, j \neq i)$ with $y_j^0 < k_j$. The solution $(y_1^0 = 0, y_2^0 = a_2)$, with $k_2 \leq a_2 < 1$, automatically satisfies $F_1(y_1, y_2) = 0$ and is an equilibrium if and only if it also satisfies $F_2(y_1, y_2) = 0$. This occurs when

$$(2.10) \qquad c_2 \left(1 - a_2 \right) \beta_{22} c_2 S_2^0 w_2(a_2) = (\mu + \gamma_2) N^0,$$

or $H_2(a_2) = 1$. Since $H_i'(x) < 0$, for $0 \leq x < 1$, and $H_i(1) = 0$, there exists a unique solution a_2 of (2.10) with $k_2 \leq a_2 < 1$ if and only if $H_2(k_2) \geq 1$. Solve (2.10) for a_2; $(0, y_2^0) = (0, a_2)$ is desired.

The proof of the existence of the boundary equilibrium $(y_1^0, 0)$, where $k_1 \leq y_1^0 < 1$, is similar.

(2) It suffices to show that $(0, y_2^0 \geq k_2)$ is stable if $R_1(0) < 1$ and unstable if $R_1(0) > 1$.

Denote the Jacobian matrix at $(0, y_2^0)$ by J_2. Then

$$J_2 = \begin{pmatrix} j_{11} & S_1^0 \dfrac{c_1 c_2}{N^0} \beta_{12} h(0) g'(y_2^0) y_2^0 \\ 0 & j_{22} \end{pmatrix},$$

where

$$j_{11} = -\left(\mu + \gamma_1 \right) + S_1^0 \frac{c_1^2}{N^0} \beta_{11} w_1(0) = (\mu + \gamma_1) \left(R_1(0) - 1 \right),$$

$$j_{22} = -\left(\mu + \gamma_2 + \lambda_2 \right) + \left(1 - y_2^0 \right) \frac{c_2^2}{N^0} \beta_{22} S_2^0 \left(w_2(y_2^0) + w_2'(y_2^0) \right).$$

Hence the eigenvalues are $\rho_1 = j_{11}$ and $\rho_2 = j_{22}$. Because $(0, y_2^0)$ is an equilibrium,

$$(\mu + \gamma_2 + \lambda_2) \, y_2^0 = \lambda_2.$$

Hence

$$\rho_2 = -y_2^0 \frac{c_2^2}{N^0} \beta_{22} S_2^0 w_2(y_2^0) + \left(1 - y_2^0\right) \frac{c_2^2}{N^0} \beta_{22} S_2^0 w_2'(y_2^0) y_2^0 < 0.$$

The stability is determined by the sign of ρ_1, and the conclusion immediately follows.   □

The following lemma is needed to establish the global stability of the non-infection-free equilibria.

LEMMA 2.7. (1) *The region $0 \le y_i \le k_i$, $i = 1, 2$, is a global attractor for (2.4) in the nonnegative first quadrant if $H_i(k_i) < 1$ for both $i = 1$ and $i = 2$.*

(2) *The region $0 \le y_i \le k_i$ and $k_j \le y_j \le 1$ is a global attractor for (2.4) in the nonnegative first quadrant if $H_i(k_i) < 1 \le H_j(k_j)$.*

(3) *The region $k_i \le y_i \le 1$, $i = 1, 2$, is a global attractor for (2.4) in the nonnegative first quadrant if $H_i(k_i) \ge 1$ for both $i = 1$ and $i = 2$.*

Proof. We rewrite equation (2.4) as

$$(2.11) \qquad \frac{dy_i}{dt} = -(\mu + \gamma_i) \, y_i \, (1 - H_i(y_i)) + \frac{c_i(1 - y_i)}{N^0} \beta_{ij} c_j S_j^0 h(y_1) g(y_2) y_j.$$

(1) Suppose $H_i(k_i) < 1$. Then, since H_i is decreasing, $H_i(y_i) < 1$ for all $y_i \ge k_i$. Hence

$$\frac{dy_i}{dt} = -(\mu + \gamma_i) \, y_i \, (1 - H_i(y_i)) < 0$$

for all $y_i \ge k_i$. In addition to Lemma 2.2, the conclusion follows.

(2) If $H_i(k_i) < 1 \le H_j(k_j)$, we still have $\frac{dy_i}{dt} < 0$ for all $y_i \ge k_i$, but it follows from $1 \le H_j(k_j)$ that $H_j(y_j) > 1$ for all $0 \le y_j < k_j$. Hence $\frac{dy_j}{dt} > 0$, and, based on Lemma 2.2, the region $0 \le y_i \le k_i$ and $k_j \le y_j \le 1$ is a global attractor for (2.4) in the nonnegative first quadrant.

(3) The proof is similar.   □

We now give a complete analysis of the model dynamics.

THEOREM 2.8. (1) *Suppose $H_i(k_i) < 1$ for both $i = 1$ and $i = 2$, so that neither boundary equilibrium exists. Then, if $R_0 < 1$, there is no positive endemic equilibrium and the infection-free equilibrium is globally stable. If $R_0 > 1$, there exists a unique endemic equilibrium $(0 < y_1^* < k_1, 0 < y_2^* < k_1)$, which is globally stable.*

(2) *Assume that $H_i(k_i) \ge 1$, for both $i = 1$ and $i = 2$, so that both boundary equilibria exist. Then they must be both unstable.*

(3) *If $H_i(k_i) \ge 1$ and $R_j(0) < 1$, so that the boundary equilibrium $(y_i^0 \ge k_i, y_j^0 = 0)$, $j \ne i$, exists and is stable, then there is neither other boundary equilibrium nor endemic equilibrium, and this boundary equilibrium is globally stable.*

(4) *If $H_i(k_i) \ge 1$ and $H_j(k_j) < 1 < R_j(0)$, so that there exists only one boundary equilibrium, $(y_i^0 \ge k_i, y_j^0 = 0)$, $j \ne i$, and it is unstable, then there exists a unique endemic equilibrium $(k_i \le y_i^* < 1, 0 < y_j^* < k_j)$, which is globally stable.*

(5) *Assume $H_i(k_i) \ge 1$, for both $i = 1$ and $i = 2$, so that two unstable boundary equilibria exist. Then there exists a unique positive endemic equilibrium with $k_i \le y_i^* < 1$, $i = 1, 2$, which is globally stable.*

Proof. (1) First we show that if $H_i(k_i) < 1$, the curve $F_i(y_1, y_2) = 0$ does not go through the region $(y_1 \geq k_1, y_2 \geq k_2)$. In fact, a point (y_1, y_2) is on this curve if and only if it satisfies

$$(2.12) \qquad c_i\,(1 - y_i)\,\beta_{ij}c_j S_j^0 h(y_1)g(y_2)y_j = (\mu + \gamma_i)\,N^0 y_i\,(1 - H_i(y_i))$$

for $j \neq i$.

If $y_1 \geq k_1$ or $y_2 \geq k_2$, the left-hand side of (2.12) could be zero, but the right-hand side must be positive because $H_i(x)$ is a decreasing function, and $H_i(k_i) < 1$. Hence $F_i(y_1, y_2) = 0$ cannot pass through the region $(y_1 \geq k_1, y_2 \geq k_2)$.

Next we consider $F_1 = 0$, for $0 \leq y_1 < k_1$, or

$$(2.13) \qquad \frac{(1 - H_1(y_1))(\mu + \gamma_1)N^0 y_1}{c_1(1 - y_1)\beta_{12}c_2 h(y_1)} = g(y_2)y_2.$$

Suppose that $R_1(0) < 1$. Then (2.13) defines a curve lying completely in the first nonnegative quadrant joining the points $(0,0)$ and $(0, k_2)$. Similarly, if $R_2(0) < 1$, $F_2 = 0$ defines a curve lying completely in the first nonnegative quadrant joining the points $(0,0)$ and $(k_1, 0)$.

If $R_0 < 1$, then both $R_i(0)$ must be less than one, and hence both curves $F_i = 0$ lie in the first nonnegative quadrant joining the points $(0,0)$ and $(y_i = 0, y_j = k_j)$. As shown in the proof of Theorem 4.1 [10], the curve $F_1 = 0$ now lies above $F_2 = 0$ as y_i, $i = 1, 2$, greater than and near zero. It follows from Lemma 2.4 that there is no positive intersection point of $F_1 = 0$ and $F_2 = 0$ in the region $0 < y_i < k_i$, $i = 1, 2$. Also because the curves $F_i = 0$, $i = 1, 2$, do not go through $y_i \geq k_i$, there is no positive endemic equilibrium in the first quadrant. Therefore, the local stability of the infection-free equilibrium leads to its global stability from Lemmas 2.3 and 2.7.

If $R_0 > 1$, $R_i(0)$ can be both less than one, one of them greater than one, or both greater than one. If $R_i(0) < 1$, for both $i = 1$ and $i = 2$, again, both curves $F_i = 0$ lie in the first nonnegative quadrant joining the points $(0,0)$ and $(y_i = 0, y_j = k_j)$. Then it follows from the proof of Theorem 4.1 [10] that the curve $F_1 = 0$ lies below $F_2 = 0$ as y_i, $i = 1, 2$, greater than and near zero. Hence there exists at least one intersection point of $F_1 = 0$ and $F_2 = 0$ in the region $0 < y_i < k_i$, $i = 1, 2$. The uniqueness then follows from Lemma 2.4.

Suppose that $R_0 > 1$ but that there exists at least one $R_i(0) > 1$. Without loss of generality, we assume $R_1(0) > 1$. Then it follows from (2.13) that the curve $F_1 = 0$ goes to the fourth quadrant when y_1 is greater than and near zero. As y_1 increases, $F_1 = 0$ passes through $(\tilde{y}_1, 0)$, where $\tilde{y}_1$ satisfies $H_1 = 0$, goes back to the first nonnegative quadrant, and then joins $(\tilde{y}_1, k_2)$. Hence for either $R_2(0) < 1$ or $R_2(0) > 1$, there always exists an intersection point of $F_1 = 0$ and $F_2 = 0$ in the region $0 < y_i < k_i$, $i = 1, 2$. This endemic equilibrium is unique because of Lemma 2.4. The local stability can be obtained from the Jacobian at this point (see [10]), and again its local stability leads to its global stability.

(2) Since $H_i(x)$, $i = 1, 2$, are decreasing functions for $0 \leq x < 1$,

$$H_i(k_i) < H_i(0) = R_i(0).$$

It follows from $H_i(k_i) \geq 1$ that $R_i(0) > 1$ for $i = 1, 2$. Hence both boundary equilibria are unstable from Lemma 2.6.

(3) Assume that $(0, y_2^0)$ exists and is stable. Then the nonexistence of $(y_1^0, 0)$ is a direct consequence of (2). We need only to show that there exists no positive endemic equilibrium.

Since $(y_1^0, 0)$ does not exist, $H_1(k_1) < 1$. It follows from the same argument in the proof of (1) that $F_1(y_1, y_2) = 0$ has no solution for $y_1 \geq k_1$. Hence there is no endemic equilibrium in the region $k_1 \leq y_1 < 1$.

Next we consider the region $0 < y_1 < k_1$ and $k_2 \leq y_2 \leq 1$. Since $(0, y_2^0)$ is stable, $R_1(0) < 1$, which leads to

$$H_1(y_1) < H_1(0) = R_1(0) < 1$$

for all $0 < y_1 < k_1$. Hence for each $k_2 \leq a_2 \leq 1$, $F_1(y_1, a_2) = 0$ has no solution for all $0 < y_1 < k_1$, and the curve $F_1(y_1, y_2) = 0$ intersects the horizontal line $y_2 = a_2$ only along the y_2-axis for $k_2 \leq a_2 \leq 1$. That is, the curve $F_1(y_1, y_2) = 0$ lies completely on the y_2-axis for $k_2 \leq y_2 \leq 1$ and does not go through the region $0 < y_1 < k_1$ or $k_2 \leq y_2 \leq 1$.

Now we show that the curve $F_2(y_1, y_2) = 0$ does not go through the region $0 < y_i < k_i$, $i = 1, 2$. As shown in (1), a point (y_1, y_2) is on this curve if and only if it satisfies (2.12) for $i = 2$ and $j = 1$. However, for $0 < y_2 < k_2$, we have $H_2(y_2) > H_2(k_2) \geq 1$. Then (2.12) does not hold for $i = 2$. That is, the curve $F_2(y_1, y_2) = 0$ does not go through the region $0 < y_i < k_i$, $i = 1, 2$. With the locations of $F_1(y_1, y_2) = 0$ and $F_2(y_1, y_2) = 0$ shown above, there exists no positive endemic equilibrium.

(4) Suppose that $H_2(k_2) \geq 1$ and $R_1(0) > 1 > H_1(k_1)$. Then $(0, y_2^0 \geq k_2)$ exists, but is unstable, and $(y_1^0 > k_1, 0)$ does not exist.

It follows from $H_1(k_1) < 1 < R_1(0) = H_1(0)$ that there exists a unique $0 < y_1^* < k_1$ such that $H_1(y_1^*) = 1$. Hence (y_1^*, y_2) satisfies $F_1 = 0$ for any $y_2 \geq k_2$ from (2.12).

Since $H_2(k_2) \geq 1$ and $H_2(1) = 0$, there exists a unique $y_2^* \geq k_2$ such that $H_2(y_2^*) = 1$. Therefore, $(0 < y_1^* < k_1, k_2 \leq y_2^* < 1)$ is a positive endemic equilibrium.

The proof that (2.12), for $i = 1$, does not hold for $y_1 \geq k_1$ and $y_2 < k_2$ is similar to the proof of (3). It follows from $H_1(k_1) < 1$ that $H_1(y_1) < 1$ for all $y_1 \geq k_1$, and from $H_2(k_2) \geq 1$ that $H_2(y_2) > 1$ for all $y_2 < k_2$. Hence $(0 < y_1^* < k_1, k_2 \leq y_2^* < 1)$ is the unique positive endemic equilibrium.

Since $(0, y_2^0)$ is unstable $(R_1(0) > 1)$, the infection-free equilibrium is unstable, and the positive endemic equilibrium is locally stable following from the eigenvalues of their Jacobian matrices [10]. Again, the local stability of the endemic equilibrium then leads to its global stability.

(5) First, it follows from $R_i(0) > H_i(k_i) \geq 1$, $i = 1, 2$, that the two diagonal elements of the Jacobian matrix at the infection-free equilibrium are positive [10]. Hence the infection-free equilibrium is unstable.

Next we show that there exists a unique positive endemic equilibrium. The point (y_1, y_2) is a positive endemic equilibrium if and only if it satisfies (2.12) for $i = 1, 2$. Let $y_i \geq k_i$. Then the second term of the left-hand side in (2.12) vanishes. Hence $(y_1 \geq k_1, y_2 \geq k_2)$ is a positive endemic equilibrium if and only if it satisfies $H_i(y_i) = 1$ for both $i = 1$ and $i = 2$. It follows from $H_i(k_i) \geq 1$ and $H_i(1) = 0$ that there exists a unique solution y_i^* for each $H_i(y_i) = 1$ in the region $y_i \geq k_i$. Then (y_1^*, y_2^*) is an endemic equilibrium. With the same argument as in the proof of (4), there is no positive endemic equilibrium in the region $(0 < y_i < k_i)$. Therefore, $(k_2 \leq y_1^*, k_2 \leq y_2^*)$ is the unique positive endemic equilibrium in the first quadrant.

Finally, the local stability of the positive endemic equilibrium follows from location of the eigenvalues of the Jacobian at this point. (Details can be found in the proof of Theorem 4.2 [10].) The global stability follows again from Lemmas 2.3 and 2.7. □
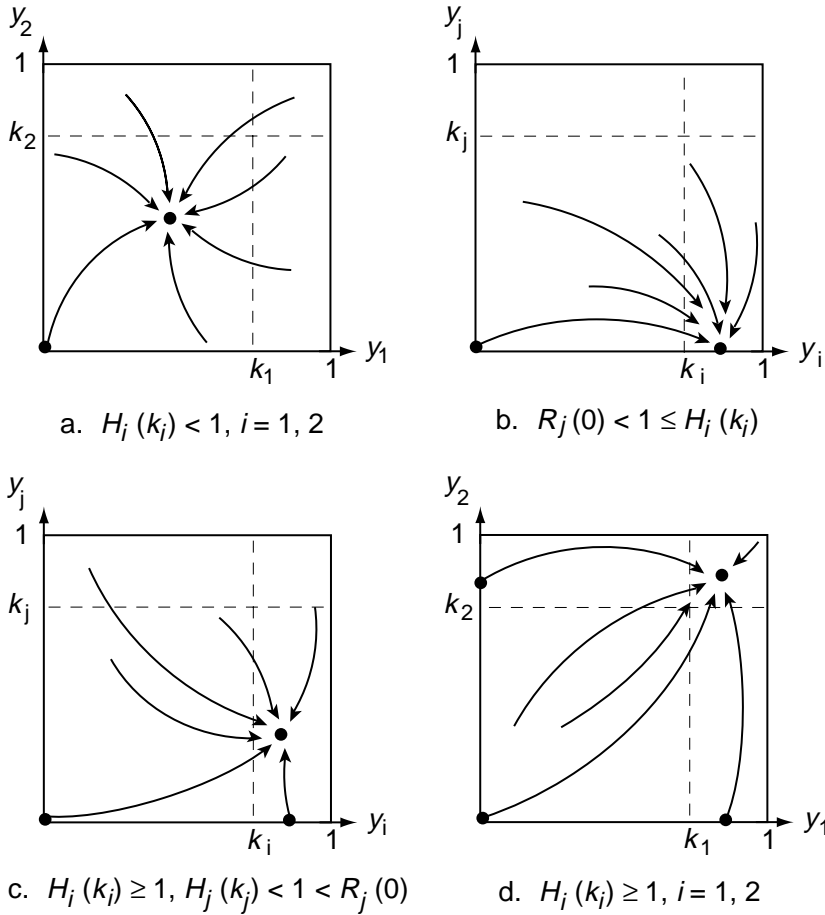
FIG. 2.1. (a) *For $R_0 > 1$, if $H_i(k_i) < 1$ for both $i = 1$ and $i = 2$, there exists a unique endemic equilibrium $(0 < y_1^* < k_1, 0 < y_2^* < k_2)$ in the nonnegative first quadrant, and it is globally stable. (b) If $H_i(k_i) \geq 1$ and $H_j(k_j) < 1$, $j \neq i$, the boundary equilibrium $(y_i^0 > 0, y_j^0 = 0)$ is unique. In addition, if $R_j(0) < 1$, this boundary equilibrium is globally stable in the nonnegative first quadrant. (c) This boundary equilibrium is unstable provided $R_j(0) > 1$, and a globally stable, positive endemic equilibrium with $k_i \leq y_i^* < 1$ and $0 < y_j^* < k_j$, $j \neq i$, appears. (d) If $H_i(k_i) \geq 1$, for both $i = 1$ and $i = 2$, the positive endemic equilibrium $(k_1 \leq y_1^* < 1, k_2 \leq y_2^* < 1)$ is the only equilibrium in the positive quadrant, and it is a global attractor in the nonnegative first quadrant.*

In summary, from Theorem 2.8, four different kinds of equilibria may exist in the nonnegative first quadrant including the boundary axes under hypothesis (2.9), and there is always only one stable equilibrium, and the stability is global. The dynamical behavior of these equilibria are summarized in Figure 2.1. If $R_0 < 1$, the infection-free equilibrium is the only equilibrium in the nonnegative first quadrant and is globally stable. That is, all orbits starting in the nonnegative first quadrant approach this infection-free equilibrium as $t \to \infty$. For $R_0 > 1$, the infection-free equilibrium becomes unstable, and if $H_i(k_i) < 1$ for both $i = 1$ and $i = 2$, there exists a unique

endemic equilibrium $(0 < y_1^* < k_1, 0 < y_2^* < k_2)$ in the nonnegative first quadrant, and it is globally stable (Figure 2.1a). Moreover, if $H_i(k_i) \geq 1$ and $H_j(k_j) < 1$, $j \neq i$, the boundary equilibrium $(y_i^0 > 0, y_j^0 = 0)$ is the only boundary equilibrium. In addition, if $R_j(0) < 1$, this boundary equilibrium is globally stable in the nonnegative first quadrant (Figure 2.1b). This boundary equilibrium is unstable provided $R_j(0) > 1$ and, if this happens, a globally stable, positive endemic equilibrium with $k_i \leq y_i^* < 1$ and $0 < y_j^* < k_j$, $j \neq i$, appears (Figure 2.1c). Finally, if $H_i(k_i) \geq 1$, for both $i = 1$ and $i = 2$, then the positive endemic equilibrium $(k_1 \leq y_1^* < 1, k_2 \leq y_2^* < 1)$ is the only equilibrium in the positive quadrant, and it is a global attractor in the nonnegative first quadrant (Figure 2.1d).

3. Effects of behavior changes. We have investigated the effect that behavior changes can have on the transmission dynamics of a two-group STD epidemic model. We have shown (section 2.2) that if people significantly reduce their partnership formations within their own group but continue to have intergroup partnerships, then if the reproductive number is less than one, the epidemic dies out. If the reproductive number exceeds one, the epidemic approaches an endemic steady state regardless of the initial infection status of the population. These transmission dynamics are qualitatively the same as those in [10], where all desirability and acceptability functions are assumed to be strictly positive.

However, if people modify their behavior dramatically in intergroup partnership formations such that when the infection level in the other group gets sufficiently high, they completely stop forming partners with people in that group, then the groups can be completely isolated, and the epidemic may be eradicated in one group but continue to exist in the other group (section 2.3).

We use the function $H_i(k_i)$ to characterize the level of the infection in group i and the response of people in the group j to the infection in group i.

If $H_i(k_i) < 1$ for both $i = 1$ and $i = 2$, the infection levels in both groups are low so that people in neither group stop forming intergroup partnerships. Because of the persistent intergroup partnership formations, a boundary equilibrium cannot exist. However, since the infection levels are low, the endemic level of the epidemic is also low: $y_i^* < k_i^*$ (Figure 2.1a), compared with $y_i^* \geq k_i$ when both $H_i(k_i) \geq 1$ (Figure 2.1d).

If $H_i(k_i) \geq 1$, the infection level in group i exceeds a critical value, and people in group j stop forming partners with them. This isolates group j from group i, and the boundary equilibrium $(y_i^0 > 0, y_j^0 = 0)$ exists.

However, this behavior change does not necessarily eradicate the epidemic in group j. The group reproductive number $R_j(0)$ characterizes the epidemic reproduction within the group in the absence of intergroup partnership formations. Whether the epidemic will be eradicated will be determined by the group reproductive number. If the group reproductive number in group j, $R_j(0)$, is greater than one, the epidemic still spreads in the two groups. The epidemic can be completely eradicated in group j only if $R_j(0) < 1$ (Figure 2.1b). That is, people in group j need not only to stop forming partners with people in the highly infected group i, but also to reduce the infection production in their own group in order to completely eradicate the epidemic in the group. Nevertheless, when people in group j do not modify their behavior to a level that will completely eradicate the epidemic in their group, the behavior changes still reduce the endemic epidemic level to $y_j^* < k_j$ (Figure 2.1c).

The intergroup partnership formation plays a more important role in the transmission of the epidemic. As shown above, the epidemic may be eradicated in a group

only if the group reproductive number in that group is less than one, provided people in two groups are isolated.

However, even if both group reproductive numbers $R_i(0)$ are less than one, the epidemic may still persist. This can be seen from either the expression of the reproductive number in (2.5), the Jacobian at the infection-free equilibrium, or the fact that $H_i(k_i) < R_i(0)$ implies the nonexistence of boundary equilibria and the existence of a globally stable endemic equilibrium proved in Theorem 2.8(1) (Figure 2.1a). When this happens, although the epidemic persists in the population, the behavior changes can still drive the endemic epidemic to very small values. The number k_i measures people's behavior changes responding to higher infection levels; the smaller k_i is, the more sensitive people are in forming intergroup partners, and the lower the endemic status could reach. Under the condition that $R_i(0) < 1$ for both $i = 1$ and $i = 2$, as k_1 and k_2 approach zero, in spite of the reproductive number R_0 greater than one, the endemic level will converge to zero.

Because two stable boundary equilibria cannot coexist, changing the desirability and acceptability formation cannot eradicate the epidemic in the entire population once the epidemic exceeds the epidemic threshold. The only way to stop the epidemic eventually is through behavior changes that reduce the reproductive number for the entire population below one so that any infection introduced into the group population will die out. These effective changes include reducing the number of contacts (reducing c_i) or reducing the infectivity (reducing β_{ij}) by using safe sex practices. A recent survey [18] showed that 7 percent of young homosexual and bisexual men in the United States are infected with HIV, and that more than a third of them have had unprotected sex in the past six months. That is, even though the seriousness of HIV infection is well known, this knowledge has not reduced high-risk behavior in a social group with a high reproductive number. To slow, and it is hoped to stop, the epidemic will require dramatic behavior changes beyond the current trend.

There are some unusual features of the model that should be addressed. In multigroup STD models, usually, when the infection-free equilibrium loses its stability, either a unique endemic equilibrium becomes globally stable (see, e.g., [3]) or multiple endemic equilibria may appear [8, 14]. The existence of the boundary equilibrium is unusual for a system of two ordinary differential equations modeling STDs. Moreover, the phase plane diagram, shown in Figure 2.1d, is also unusual. When the infection-free equilibrium bifurcates into a positive endemic equilibrium and two boundary equilibria by a Hopf pitchfork bifurcation, one would expect the possibility that the endemic equilibrium is unstable, but the two boundary equilibria are both locally stable. When this occurs, the transmission dynamics depend on initial infections from which solution trajectories can go to either boundary equilibrium. However, in this model, whenever the boundary equilibria exist, they are always unstable, and all initially infected populations converge to the unique endemic equilibrium.

Even though the model investigated in this paper is a simple SIS model, we can use it to gain some insight into STD epidemics such as gonorrhea or syphilis. For example if the STD were more easily transmitted within a homosexual population than a heterosexual population so that the reproductive number for the heterosexual population "group" is less than one, and the group reproductive number for the male homosexual population "group" is greater than one, then as long as the epidemic persists in the male homosexual population, and there are bisexual men transmitting the infection between the two groups, the infection will continue to persist in the heterosexual population. However, because the heterosexual group reproductive

number is small, these few infections will quickly die out and do not pose the threat of increasing the reproductive number for the heterosexual population and fueling a widespread epidemic. Also, the instability of the boundary equilibria indicates that isolation/quarantine policies such as a ban on the immigration of people infected with an STD or the attempt to quarantine all the STD-infected people are not effective strategies for preventing an STD epidemic.

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